SEQUENCE LISTING
(1) GENERAL INFORMATION:
(1) APPLICANT: Shyjan, Andrew W.
(11) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF TUMO PROGRESSION
(111) NUMBER OF SEQUENCES: 9
(iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Fish & Richardson P.C. (B) STREET: 225 Franklin Street (C) CITY: Boston (D) STATE: MA (E) COUNTRY: USA (F) ZIP: 02110-2804
(v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: Patentin Release #1.0, Version #1.30
(vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US (B) FILING DATE: 29-MAR-1996 (C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 08/12,431 (B) FILING DATE: 29-MAR-1995
(viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Fasse, J. Peter (B) REGISTRATION NUMBER: 32,983 (C) REFERENCE/DOCKET NUMBER: 07334/004001
(ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 617/542-5070 (B) TELEFAX: 617/542-8906 (C) TELEX: 200154
(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 186 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGTGCTGGAG TACCTCATGG GCGGTGCCTA CCGCTGCAAC TACACTCGGA AAAGCTTCCG 60 GACTOTOTAC AACAACTTGT TTGGCCCTAA GAGGGTAGAG CTCAGCAGAC AQACAGTGTC 120

CTGTGCCTCC CAGAGTAACA TGTGGTTCCT TGATGTGCTT CCCCAAAAGC CCACCTGTGC	180
AGAATG	186
(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2729 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
AAGGAGGCTA GGCTGCACCC TTCCCGCTTG CTCAGCAGCT GAGGCAGGGT CAGAAAGCAT	60
GGATAGAGAA GACATTTTGC AAAAGGGAAT GCATCTTTGT AATTCCCAGT ACAAAAGACC	120
CTAACAGATG TTGCTGTGGT CAGCTCACTA ACCAGCACAT CCCCCCTTTG CCGAGTGGGG	180
CTCCCAGCAC AACAGGAGAG GACACCAAGC AGGCAGACAC GCAGTCCGGG AAATGGTCTG	240
TCAGCAAACA CACCCAGAGC TACCCAACAG ACTCCTATGG GATTCTTGAA TTCCAGGGTG	300
GGGGTTACTC CAATAAAGCC ATG TAC ATC CGA GTC TCC TAC GAC ACC AAG Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys 1 5 10	350
CCA GAT TCC CTG CTC CAC CTC ATG GTG AAG GAC TGG CAG CTG GAG CTC Pro Asp Ser Leu His Leu Met Val Lys Asp Trp Gln Leu Glu Leu 15 20 25	398
CCG AAG CTC TTG ATA TCT GTG CAC GGA GGC CTC CAA AGC TTC GAG ATG Pro Lys Leu Leu Ile Ser Val His Gly Gly Leu Gln Ser Phe Glu Met 30 35 40	446
CAG TCC AAA CTG AAG CAG GTG TTT GGG AAA GGT CTG ATC AAG GCT GCC Gln Ser Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile Lys Ala Ala 45	494
ATG ACC ACG GGG GCG TGG ATC TTC ACC GGG GGT GTG AGC ACT GGT GTC Met Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val 60 65 70	542
GTC AGC CAT GTG GGG GAT GCC TTG AAA GAC CAC TCC TCC AAG TCC AGA Val Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg 75 80 85 90	590
GGC CGG CTC TGT GCT ATA GGA ATT GCT CCC TGG GGC ATG GTG GAG AAC Gly Arg Leu Cys Ala Ile Gly Ile Ala Pro Trp Gly Met Val Glu Asn 95	638
AAG GAA GAC CTG ATT GGA AAA GAT GTA ACA AGA GTC TAT CAG ACC ATG Lys Glu Asp Leu Ile Gly Lys Asp Val Thr Arg Val Tyr Gln Thr Met 110	68 6
TCC AAC CCT CTG AGC AAG CTC TCT GTG CTC AAC AAT TCC CAC ACT CAC	734

125	i	130		13	35	
TTC ATC TTG Phe Ile Leu 140	GCT GAC AAG Ala Asp Ass	GGC ACC Gly Thr 145	CTG GGC Leu Gly	AAG TAT GG Lys Tyr Gl 150	ST GCT GAG Ly Ala Glu	GTG 782 Val
AAG CTT CGA Lys Leu Arg 155	AGA CAG CTG Arg Gln Leu 160	Glu Lys	CAC ATC His Ile	TCC CTG CA Ser Leu Gl 165	AG AAG ATC In Lys Ile	AAC 830 Asn 170
ACA AGG CTG Thr Arg Leu	GGC CAG GGT Gly Gln Gly 175	GTA CCT Val Pro	GTC GTG Val Val 180	GGC CTA GT Gly Leu Va	CG GTA GAA 11 Val Glu 185	GGT 878 Gly
GGT CCT AAC Gly Pro Asn	GTG GTT TCT Val Val Ser 190	ATC GTC	CTG GAG Leu Glu 195	TAT CTC AA Tyr Leu Ly	A GAA GAC 78 Glu Asp 200	CCT 926 Pro
CCT GTC CCT Pro Val Pro 205	GTG GTG GTT Val Val Val	TGC GAT Cys Asp 210	GGC AGT Gly Ser	GGA CGT GC Gly Arg Al 21	a Ser Asp	ATT 974 Ile
TTG TCC TTC Leu Ser Phe 220	GCA CAC AAI Ala His Lys	TAC TGC Tyr Cys 225	GAC GAA Asp Glu	GGA GGA GT Gly Gly Va 230	CC ATA AAC	GAG 1022 Glu
TCC CTG CGG Ser Leu Arg 235	GAC CAG CTT Asp Gln Let 240	Leu Val	ACC ATT Thr Ile	CAG AAA AC Gln Lys Th 245	A TTT AAT Ar Phe Asn	TAC 1070 Tyr 250
AGC AAG TCC Ser Lys Ser	CAG TCG TATE Cln Ser Type 255	CAG CTG	TTT GCA Phe Ala 260	ATT ATC AT Ile Ile Me	G GAG TGC t Glu Cys 265	ATG 1118 Met
AAG AAG AAA Lys Lys Lys	GAA CTC GTC Glu Leu Val 270	ACT GTG Thr Val	TTT CGG Phe Arg 275	ATG GGT TO Met Gly Se	CC GAG GGT er Glu Gly 280	CAG 1166 Gln
CAA GAT GTC Gln Asp Val 285	GAG ATG GCI Glu Met Ala	ATT TTA Ile Leu 290	ACT GCC Thr Ala	TTG CTC AA Leu Leu Ly 29	s Gly Thr	AAC 1214 Asn
GCA TCA GCT Ala Ser Ala 300	CCA GAT CAC Pro Asp Gli	CTG AGC Leu Ser 305	TTG GCC Leu Ala	CTG GCT TG Leu Ala Tr 310	G AAC CGG p Asn Arg	GTC 1262 Val
GAC ATA GCG Asp Ile Ala 315	CGA AGC CAC Arg Ser Glr 320	Ile Phe	GTC TTT Val Phe	GGC CCA CA Gly Pro Hi 325	C TGG CCG	CCA 1310 Pro 330
CTG GGA AGC Leu Gly Ser	CTG GCC CCT Leu Ala Pro 335	CCT GTG Pro Val	GAC ACC Asp Thr 340	AAA GCC GC Lys Ala Al	A GAG AAG A Glu Lys 345	GAA 1358 Glu
AAG AAG CCA Lys Lys Pro	CCC ACA GCC Pro Thr Ala 350	ACC ACC Thr Thr	AAG GGG Lys.Gly 355	AGA GGA AA Arg Gly Ly	A GGA AAA 'S Gly Lys 360	GGC 1406 Gly

AAG AAG AAA GGC AAA GTG AAA GAG GAA GTG GAG GAA GAG ACG GAC CCC Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Thr Asp Pro 365 370 375	1454
CCG AAG CTT GAG CTG CTC AAC TGG GTG AAT GCC CTG GAG CAA GCC ATG Arg Lys Leu Glu Leu Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met 380 385 390	1502
CTG GAT GCT CTT GTC CTA GAT CGG GTG GAC TTT GTA AAG CTC CTG ATT Leu Asp Ala Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile 400 405 410	1550
GAA AAC GGA GTG AAC ATG CAG CAT TTC CTC ACC ATC CCG AGG CTG GAG Glu Asn Gly Val Asn Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu 415 420 425	1598
GAG CTA TAC AAC ACC AGA CTG GGC CCA CCA AAC ACC CTT CAT CTG CTG Glu Leu Tyr Asn Thr Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu 430 435 440	1646
GTG CGG GAT GTA AAG AAG AGC AAC CTT CCA CCT GAT TAC CAC ATC AGC Val Arg Asp Val Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser 445 450 455	1694
CTC ATT GAT ATA GGA CTG GTG CTG GAG TAC CTC ATG GGC GGT GCC TAC Leu Ile Asp Ile Gly Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr 460 465 470	1742
CGC TGC AAC TAC ACT CGG AAA AGC TTC CGG ACT CTC TAC AAC AAC TTG Arg Cys Asn Tyr Thr Arg Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu 475 480 485 490	1790
TTT GGC CCT AAG AGG GTA GAG CTC AGC AGA CAC ACA GTG TCC TGT GCC Phe Gly Pro Lys Arg Val Glu Leu Ser Arg His Thr Val Ser Cys Ala 495 500 505	1838
TCC CAG AGT AAC ATG TGG TTC CTT GAT GTG CTT CCC CAA AAG CCC ACC Ser Gln Ser Asn Met Trp Phe Leu Asp Val Leu Pro Gln Lys Pro Thr 510 515 520	1886
TGT GCA GAA TGC AAC TCT TCA CCT CAC CTG TCC CAA ACT GAC ATC ACC Cys Ala Glu Cys Asn Ser Ser Pro His Leu Ser Gln Thr Asp Ile Thr 525 530 535	1934
CCA CCT CTG CCC T GACACCCAGT GCAGGGCCTC CTAGCTTTCA CATGCAGCCA Pro Pro Leu Pro 540	1987
TTCACATCGC CTCTCAAGAC TGGGCCAGGC AGTGCAACCT GTCAAGCATG TCTGTCCTCC	2047
CCTCCTTCCT ACANTAGCCC CCCCTCTGGG CCCCATGCCT CTGCTCTCTC AGCCCGTTCT	2107
CCTCCCCACT GATCACTGGC GCTCCTGTTG TCTTCCAAGG CAAGGAACAA GGAAAAGCAT	
CTTTTTGCCC ACAAAAGTTT AGGGCTCCCC GCTGTTCAAC CATAGCCAAC CTCACTGTAC	
ATCGGAGTCA TCCAGGCCAG CTGCCACACA CAAGCCTTCC CCACCCTATC CCAATAGACC	2287

CTATTCCTCC	ATCAAAATCA	AAGCTAACTC	CTGGCCTGCC	ACATTGCTTC	TTCTTGCTCC	2347
agcctgttaa	ACCTCCAATA	AATGTCAGAT	CTGTGGGAA	CCTTCCTCAC	TCTCACTCCA	2407
CAGTTTGTAC	AGAGAGCGAG	AGCCTCGTTT	GGTTCTACTT	ACAAGGAAGG	CTTTGTGTCT	2467
GTCTGTCCTT	CCCAACTGAC	TTCTGTTGAC	AGAAGCAGTT	TCCACATGAA	AGCGTTGACT	2527
CACCTGGATG	TTGTCATTAA	TTAATAGTGA	TACAAAATAT	TGACACTTCT	TTTCCTGCTT	2587
CTTTGTTATG	CAGCCGAAAG	CACTTAAGCT	TCTGGGAATG	GAAGTAAGTA	GGACATGTTT	2647
GTGGCAGTTT	ATTTACTATA	TATACCTTTG	TCATTCTGTG	GAAGCAAAAA	TTGCAATGTT	2707
TTCCATGAAT	AAAGCTCGTG	CC	••			2729

(2) INFORMATION FOR SEQ ID NO:3:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 542 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

 Met
 Tyr
 Ile
 Arg
 Val
 Ser
 Tyr
 Asp
 Thr
 Lys
 Pro
 Asp
 Ser
 Leu
 Leu
 Ile
 His

 Leu
 Met
 Val
 Lys
 Asp
 Trp
 Gln
 Leu
 Glu
 Leu
 Pro
 Lys
 Leu
 Leu
 Ile
 Ser

 Val
 His
 Gly
 Gly
 Leu
 Gln
 Ser
 Phe
 Glu
 Met
 Gln
 Ser
 Leu
 Lys
 Gln

 Val
 Phe
 Gly
 Leu
 Ile
 Lys
 Ala
 Ala
 Ala
 Het
 Thr
 Gly
 Ala
 Trp

 Ile
 Phe
 Thr
 Gly
 Val
 Ser
 Thr
 Gly
 Val
 Met
 Val
 Val
 Val
 Ser
 His
 Ile
 Ala
 Ile
 Ile

Val Pro Val Val Gly Leu Val Val Glu Gly Pro Asn Val Val Ser Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro Pro Val Pro Val Val Val Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu Ser Leu Arg Asp Gln Leu 225 230 235 Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Ser Lys Ser Gln Ser Tyr Gin Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Glu Leu Val Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Val Glu Met Ala Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Ala Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gin Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu Gly Ser Leu Ala Pro Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys Lys Pro Pro Thr Ala Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Leu Glu Leu Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu 385 Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met 410 Gin His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg 470 Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Val

					485					490					495			
C	lu	Leu	Ser	Arg 500	His	Thr	Val	Ser	Су в 5 05	Ala	Ser	Gln	Ser	Asn 510	Met	Trp		
I	he	Leu	Asp 515	Val	Leu	Pro	Gln	Lys 520	Pro	Thr	Сув	Ala	Glu 52 5	Сув	Asn	Ser		
5	er	Pro 530	His	Leu	Ser	Gln	Thr 535	Asp	Ile	Thr	Pro	Pro 540	Leu	Pro				
((2)	INFO	ORMA!	rion	FOR	SEQ	ID 1	NO: 4	:									
			(1 (1 (1	A) LI B) T: C) S: D) T:	engti YPE: Trani Opola	HARAC nucl nucl DEDNI OGY:) bad leic ESS: line	acio sino sar	airs i gle		-							
		(xi	SE(QUEN	CE D	ESCRI	[PTI	ON:	SEQ :	ID NO	0:4:							
C	GGG	CAAGO	CAC 1	ATCA	AGGA	AC												20
((2)	INFO	ORMA?	rion	FOR	SEQ	ID 1	NO: 5	:									
		(1)	(1 (1	A) LI B) T C) S'	engti YPE : Trani	HARAC H: 23 nucl DEDNI OGY:	3 ba: leic 255:	se pa acio sino	airs 1									
		•				ESCR		ON:	S EQ	ID NO	0:5:							
						AA AC												2:
•	(2)					SEQ										٠.		
		(±)	(1 (1 (1	A) L B) T C) S'	engti Ype: Trani	HARAC H: 49 nucl DEDNI OGY:	944) Leic ZSS:	acio sino	pai: d	rs					٠			
		(ii) MO	LECU	LE T	YPE:	DNA											
		(ix) FE (i	A) N	ame/:	KEY: ION:	CDS 346	48:	37									
		•	•			escr:												
,	~~	~ n ~~~	ATA (CCCN	TCGA	GC GC	CCG	CCCG	G GCI	AGGT	TTGA	GCT	GTGC	CCT (CTCC	ATTCC	A	60

120

CTGCTGTGGC AGGGTCAGAA ATCTTGGATA GAGAAAACCT TTTGCAAACG GGAATGTATC

TTTGTAAT	TC CTAG	CACGAA	AGACTO	TAAC	: AGG	TGTI	CI	GTGG	CCAC	TT C	CACCI	ACCAG	180
CATATCCC	cc crcr	CCAAG	TGCAA	CACCO	: AGC	:AAAA:	LATG	AAGA	\GGAJ	AG (CAAAC	AGGTG	240
GAGACTCA	GC CTGA	GAAATG	GTCTGT	rrgcc	: AAG	CACA	/CCC	AGAC	CTAC	CC A	ACAC	ATTCC	300
TATGGAGT	TC TTGA	ATTCCA	GGGTG	GCGG#	TAT	TCC	LATA	AAGO	CC AT	ot Ty	T AT	rc Le	354
CGT GTA Arg Val 5	TCC TAT Ser Tyr	GAC AC	C AAG ir Lys 10	CCA Pro	GAC Asp	TCA Ser	CTG Leu	CTC Leu 15	CAT His	CTC Leu	ATG Met	GTG Val	402
AAA GAT Lys Asp 20	TGG CAG Trp Gln	Leu G	AA CTC Lu Leu 25	CCC Pro	AAG Lys	CTC Leu	TTA Leu 30	ATA Ile	TCT Ser	GTG Val	CAT His	GGA Gly 35	450
GGC CTC Gly Leu	CAG AAC Gln Asn	TTT GI Phe Gi 40	AG ATG Lu Met	CAG Gln	CCC Pro	AAG Lys 45	CTG Leu	AAA Lys	CAA Gln	GTC Val	TTT Phe 50	GGG Gly	498
AAA GGC Lys Gly	CTG ATC Leu Ile 55	AAG GG Lys A	CT GCT la Ala	ATG Met	ACC Thr 60	ACC Thr	GG G Gly	GCC Ala	TGG Trp	ATC Ile 65	TTC Phe	ACC Thr	546
GGG GGT Gly Gly	GTC AGC Val Ser 70	ACA GO	GT GTT Ly Val	ATC Ile 75	AGC Ser	CAC His	GTA Val	GGG Gly	GAT Asp 80	GCC Ala	TTG Leu	A AA Lys	594
GAC CAC Asp His 85	TCC TCC Ser Ser	AAG TO	CC AGA er Arg 90	G GC Gly	CGG Arg	GTT Val	TGT Cys	GCT Ala 95	ATA Ile	G GA Gly	ATT	GCT Ala	642
CCA TGG Pro Trp 100	GGC ATC Gly Ile	Val G	AG AAT lu Asn 05	AAG Lys	GAA Glu	GAC Asp	CTG Leu 110	GTT Val	GGA Gly	AAG Lys	GAT Asp	GTA Val 115	690
ACA AGA Thr Arg	GTG TAC Val Tyr	CAG AGIN TI	CC ATG hr Met	TCC Ser	AAC Asn	CCT Pro 125	CTA Leu	AGT Ser	AAG Lys	CTC Leu	TCT Ser 130	GTG Val	738
CTC AAC Leu Asn	AAC TCC Asn Ser 135	His T	hr His	Phe	ATC Ile 140	CTG Leu	GCT Ala	GAC Asp	AAT Asn	GGC Gly 145	ACC Thr	CTG Leu	786
GGC AAG Gly Lys	TAT GGC Tyr Gly 150	GCC G	AG GTG lu Val	AAG Lys 155	CTG Leu	CGA Arg	AGG Arg	CTG Leu	CTG Leu 160	GAA Glu	AAG Lys	CAC His	834
ATC TCC Ile Ser 165	CTC CAG Leu Gln	AAG A Lys I	TC AAC le Asn 170	ACA Thr	AG A Arg	CTG Leu	GGG Gly	CAG Gln 175	GGC Gly	GTG Val	CCC Pro	CTC Leu	882
GTG GGT Val Gly 180	CTC GTG Leu Val	Val G	AG GGG lu Gly 85	GGC Gly	CCT Pro	AAC Asn	GTG Val 190	GTG Val	TCC Ser	ATC Ile	GTC Val	TTG Leu 195	930

G AA Glu	TAC Tyr	CTG Leu	CAA Gln	GAA Glu 200	GAG Glu	CCT Pro	CCC Pro	ATC Ile	CCT Pr 205	GTG Val	GTG Val	ATT Ile	TGT Cys	GAT Asp 210	G GC Gly	978
AGC Ser	GGA Gly	CGT Arg	GCC Ala 215	TCG Ser	GAC Asp	ATC Ile	CTG Leu	TCC Ser 220	TTT Phe	GCG Ala	CAC His	AAG Lys	TAC Tyr 225	TGT Cys	GAA Glu	1026
GAA Glu	GGC Gly	GGA Gly 230	ATA Ile	ATA Ile	AAT Asn	GA G Glu	TCC Ser 235	CTC Leu	AGG Arg	GAG Glu	CAG Gln	CTT Leu 240	CTA Leu	GTT Val	ACC Thr	1074
ATT Ile	CAG Gln 245	AAA Lys	ACA Thr	TTT Phe	AAT Asn	TAT Tyr 250	AAT Asn	AAG Lys	GCA Ala	CAA Gln	TCA Ser 255	CAT His	CAG Gln	CTG Leu	TTT Phe	1122
GCA Ala 260	ATT Ile	ATA Ile	ATG Met	GAG Glu	TGC Cys 265	ATG Met	AAG Lys	AAG Lys	AAA Lys	GAA Glu 270	CTC Leu	GTC Val	ACT Thr	GTG Val	TTC Phe 275	1170
AG A Arg	ATG Met	GGT Gly	TCT Ser	GAG Glu 280	GGC Gly	CAG Gln	CAG Gln	GAC Asp	ATC Ile 285	GAG Glu	ATG Met	GCA Ala	ATT Ile	TTA Leu 290	ACT Thr	1218
GCC Ala	CTG Leu	CTG Leu	AAA Lys 295	GGA Gly	ACA Thr	AAC Asn	GTA Val	TCT Ser 300	GCT Ala	CCA Pro	GAT Asp	CAG Gln	CTG Leu 305	AGC Ser	TTG Leu	1266
GCA Ala	CTG Leu	GCT Ala 310	TGG Trp	AAC Asn	CGC Arg	GTG Val	GAC Asp 315	ATA Ile	GCA Ala	CGA Arg	AGC Ser	CAG Gln 320	ATC Ile	TTT Phe	GTC Val	1314
TTT Phe	GGG Gly 325	CCC Pro	CAC His	TGG	ACG Thr	CCC Pro 330	CTG Leu	GGA Gly	AGC Ser	CTG	GCA Ala 335	CCC Pro	CCG Pro	ACG Thr	GAC Asp	1362
AGC Ser 340	Lys	GCC Ala	ACG Thr	G AG Glu	AAG Lys 345	GA G Glu	AAG Lys	AAG Lys	CCA Pro	CCC Pro 350	ATG Met	GCC Ala	ACC Thr	ACC Thr	AAG Lys 355	1410
GGA Gly	GGA Gly	AGA Arg	GGA Gly	AAA Lys 360	GGG Gly	AAA Lys	GGC Gly	AAG Lys	AAG Lys 365	AAA Lys	GGG Gly	AAA Lys	GTG Val	AAA Lys 370	GA G Glu	1458
G AA Glu	GTG Val	GAG Glu	GAA Glu 375	GAA Glu	ACT	GAC Asp	CCC Pro	CGG Arg 380	AAG Lys	ATA Ile	GAG Glu	CTG Lau	CTG Leu 385	AAC Asn	TGG Trp	1506
G TG Val	AAT Asn	GCT Ala 390	Leu	GAG Glu	CAA Gln	GCG Ala	ATG Met 395	CTA Leu	GAT Asp	GCT Ala	TTA Leu	GTC Val 400	TTA Leu	GAT Asp	CGT Arg	1554
GTC Val	GAC Asp 405	Phe	GTG Val	AAG Lys	CTC Leu	CTG Leu 410	ATT	GAA Glu	AAC Asn	GGA Gly	GTG Val 415	AAC Asn	ATG Met	CAA Gln	CAC His	1602
TTT Phe	CTG Leu	ACC Thr	ATT Ile	CCG Pro	AGG Arg	CTG Leu	GAG Glu	GAG Glu	CTT	TAT Tyr	AAC Asn	ACA Thr	AG A Arg	CTG Leu	GGT Gly	1650

420	425		430	435
CCA CCA AAC	ACA CTT CAT Thr Leu His 440	CTG CTG GTG	AGG GAT GTG AAA Arg Asp Val Lys 445	AA AGC AAC 1698 Lys Ser Asn 450
Leu Pro Pro	GAT TAC CAC Asp Tyr His 455	ATC AGC CTC Ile Ser Leu 460	C ATA GAC ATC GGG 1 Ile Asp Ile Gly	CTC GTG CTG 1746 Leu Val Leu 465
GAG TAC CTC	ATG GGA GGA Met Gly Gly	GCC TAC CGC Ala Tyr Arg 475	TGC AAC TAC ACT Cys Asn Tyr Thr 480	CGG AAA AAC 1794 Arg Lys Asn
TTT CGG ACC Phe Arg Thr 485	CTT TAC AAC Leu Tyr Asr	AAC TTG TTI Asn Leu Phe 490	GGA.CCA AAG AGG Gly Pro Lys Arg 495	CCT AAA GCT 1842 Pro Lys Ala
CTT AAA CTT Leu Lys Leu 500	CTG GGA ATG Leu Gly Met 505	Glu Asp Asp	GAG CCT CCA GCT Glu Pro Pro Ala 510	AAA GGG AAG 1890 Lys Gly Lys 515
AAA AAA AAA Lys Lys Lys	AAA AAG AAA Lys Lys Lys 520	AAG GAG GAA Lys Glu Glu	A GAG ATC GAC ATT 1 Glu Ile Asp Ile 525	GAT GTG GAC 1938 Asp Val Asp 530
Asp Pro Ala	GTG AGT CGG Val Ser Arg 535	TTC CAG TAT Phe Gln Tyr 540	r CCC TTC CAC GAG r Pro Phe His Glu	CTG ATG GTG 1986 Leu Met Val 545
TGG GCA GTG Trp Ala Val 550	CTG ATG AAA Leu Met Lys	CGC CAG AAA Arg Gln Lys 555	A ATG GCA GTG TTC B Met Ala Val Phe 560	CTC TGG CAG 2034 Leu Trp Gln
CGA GGG GAA Arg Gly Glu 565	GAG AGC ATC Glu Ser Met	GCC AAG GCC Ala Lys Ala 570	C CTG GTG GCC TGC a Leu Val Ala Cys 575	AAG CTC TAC 2082 Lys Leu Tyr
AAG GCC ATG Lys Ala Met 580	GCC CAC GAC Ala His Glu 585	ı Ser Ser Glu	AGT GAT CTG GTG 1 Ser Asp Leu Val 590	GAT GAC ATC. 2130 Asp Asp Ile 595
Ser Gln Asp	Lau Asp Ass	Asn Ser Lye	A GAC TTC GGC CAG B Asp Phe Gly Gln 605	Leu Ala Leu
Glu Leu Leu	GAC CAG TCG Asp Gln Ser 615	TAT AAG CAT Tyr Lys His 620	r GAC GAG CAG ATC B Asp Glu Gln Ile D	GCT ATG AAA 2226 Ala Met Lys 625
CTC CTG ACC Leu Leu Thr 630	TAC GAG CTO Tyr Glu Leu	AAA AAC TGG Lys Asn Trp 635	G AGC AAC TCG ACC p Ser Asn Ser Thr 640	TGC CTC AAA 2274 Cys Leu Lys
CTG GCC GTG Leu Ala Val 645	GCA GCC AAA Ala Ala Lys	A CAC CGG GAC His Arg Asp 650	C TTC ATT GCT CAC p.Phe Ile Ala His 655	ACC TGC AGC 2322 Thr Cys Ser

CAG Gln 660	ATG Met	CTG Leu	CTG Leu	ACC Thr	GAT Asp 665	ATG Met	TGG Trp	ATG Met	GGA Gly	AGA Arg 670	CTG Leu	CGG Arg	ATG Met	ccc Arg	AAG Lys 675	2370
AAC Asn	CCC Pro	GGC Gly	CTG Leu	AAG Lys 680	GTT Val	ATC Ile	ATG Met	GGG Gly	ATT Ile 685	CTT Leu	CTA Leu	CCC Pro	CCC	ACC Thr 690	ATC Ile	241
TTG Leu	TTT Phe	TTG Leu	GAA Glu 695	TTT Phe	CGC Arg	ACA Thr	TAT Tyr	GAT Asp 700	GAT Asp	TTC Phe	TCG Ser	TAT Tyr	CAA Gln 705	ACA Thr	TCC Ser	246
Lys	Glu	Asn 710	Glu	Asp	Gly	Lys	GAA Glu 715	Lys	Glu	Glu	Glu	Asn 720	Thr	Asp	Ala	251
Asn	Ala 725	Asp	Ala	Gly	Ser	Arg 730	AAG Lys	Gly	Asp	Glu	Glu 735	Asn	Glu	His	Lys	256:
Lys 740	Gln	Arg	Ile	Ile	Pro 745	Ile	GGA Gly	Thr	Lys	750	Сув	Lys	Phe	Tyr	Asn 755	261
Ala	Pro	Ile	Val	Lys 760	Phe	Trp	TTT Phe	Tyr	Thr 765	Ile	Ser	Tyr	Leu	Gly 770	Tyr	265
CTG Leu	CTG Leu	CTG Leu	TTT Phe 775	AAC Asn	TAC Tyr	GTC Val	ATC Ile	CTG Leu 780	GTG Val	CGG Arg	ATG Met	GAT Asp	GGC Gly 785	TGG Trp	CCG Pro	270
TCC Ser	CTC Leu	CAG Gln 790	GAG Glu	TGG Trp	ATC Ile	GTC Val	ATC Ile 795	TCC Ser	TAC Tyr	ATC Ile	GTG Val	AGC Ser 800	CTG Leu	GCG Ala	TTA Leu	275
G AG Glu	AAG Lys 805	ATA Ile	CGA Arg	G AG Glu	ATC Ile	CTC Leu 810	ATG Met	TCA Ser	GAA Glu	CCA Pro	GGC Gly 815	AAA Lys	CTC Leu	AGC Ser	CAG Gln	280
A AA Lys 820	ATC Ile	AAA Lys	GTT Val	TGG Trp	CTT Leu 825	CAG Gln	GAG Glu	TAC Tyr	TGG Trp	AAC Asn 830	ATC Ile	ACA Thr	GAT Asp	CTC	GTG Val 835	285
GCC Ala	ATT Ile	TCC Ser	ACA Thr	TTC Phe 840	ATG Met	ATT Ile	GGA Gly	GCA Ala	ATG Met 845	GCC Ala	ACG Thr	AGA Arg	TCT Ser	GTG Val 850	ATG Met	289
ATG Met	ATT	G GA Gly	AAG Lys 855	ATG Met	ATG Met	ATC Ile	GAC Asp	ATG Met 860	CTG Leu	TAC Tyr	TTT Phe	GTG Val	GTC Val 865	ATC Ile	ATG Met	294
CTG Leu	GTC Val	GTG Val 870	CTC Leu	ATG Met	AGT Ser	TTC Phe	GGA Gly 875	GTA Val	GCC Ala	CGT Arg	CAA Gln	GCC Ala 880	ATT Ile	CTG Leu	CAT His	299
C CA Pro	GAG Glu	G AG Glu	AAG Lys	CCC Pro	TCT Ser	TGG Trp	AAA Lys	CTG Leu	GCC Ala	CGA Arg	AAC Asn	ATC Ile	TTC Phe	TAC Tyr	ATG Met	304

890 895 885 CCC TAC TGG ATG ATC TAT GGA GAG GTG TTT GCA GAC CAG ATA GAC CTC 3090 Pr Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala Asp Gln Ile Asp Leu 905 910 900 TAC GCC ATG GAA ATT AAT CCT CCT TGT GGT GAG AAC CTA TAT GAT GAG 3138 Tyr Ala Met Glu Ile Asn Pro Pro Cys Gly Glu Asn Leu Tyr Asp Glu 920 GAG GGC AAG CGG CTT CCT CCC TGT ATC CCC GGC GCC TGG CTC ACT CCA 3186 Glu Gly Lys Arg Leu Pro Pro Cys Ile Pro Gly Ala Trp Leu Thr Pro GCA CTC ATG GCG TGC TAT CTA CTG GTC GCC AAC ATC CTG CTG GTG AAC 3234 Ala Leu Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn 955 CTG CTG ATT GCT GTG TTC AAC AAT ACC TTC TTT GAA GTA AAA TCA ATA 3282 Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile 970 975 TCC AAC CAG GTG TGG AAG TTC CAG CGA TAT CAG CTG ATT ATG ACA TTT 3330 Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile Met Thr Phe 990 985 CAT GAC AGG CCA GTC CTG CCC CCA CCG ATG ATC ATT TTA AGC CAC ATC 3378 His Asp Arg Pro Val Leu Pro Pro Pro Met Ile Ile Leu Ser His Ile 1000 1005 TAC ATC ATT ATG CGT CTC AGC GGC CGC TGC AGG AAA AAG AGA GAA 3426 Tyr Ile Ile Ile Met Arg Leu Ser Gly Arg Cys Arg Lys Lys Arg Glu 1020 1015 GGG GAC CAA GAG GAA CGG GAT CGT GGA TTG AAG CTC TTC CTT AGC GAC 3474 Gly Asp Gln Glu Glu Arg Asp Arg Gly Leu Lys Leu Phe Leu Ser Asp 1035 1030 GAG GAG CTA AAG AGG CTG CAT GAG TTC GAG GAG CAG TGC GTG CAG GAG 3522 Glu Glu Leu Lys Arg Leu His Glu Phe Glu Glu Gln Cys Val Gln Glu 1050 1045 CAC TTC CGG GAG AAG GAG GAT GAG CAG CAG TCG TCC AGC GAC GAG CGC 3570 His Phe Arg Glu Lys Glu Asp Glu Gln Gln Ser Ser Asp Glu Arg 1070 1060 1065 1075 ATC CGG GTC ACT TCT GAA AGA GTT GAA AAT ATG TCA ATG AGG TTG GAA 3618 Ile Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met Arg Leu Glu 1085 1080 GAA ATC AAT GAA AGA GAA ACT TIT ATG AAA ACT TCC CTG CAG ACT GTT 3666 Glu Ile Asn Glu Arg Glu Thr Phe Met Lys Thr Ser Leu Gln Thr Val 1100 GAC CTT CGA CTT GCT CAG CTA GAA GAA TTA TCT AAC AGA ATG GTG AAT 3714 Asp Leu Arg Leu Ala Gln Leu Glu Glu Leu Ser Asn Arg Met Val Asn 1115 1120 1110

GCT CTT GAA AAT	CTT GCG GGA ATC	GAC AGG TCT GAC	Leu Ile Gln Ala
Ala Leu Glu Asn	Leu Ala Gly Ile	Asp Arg Ser Asp	
1125	1130	113	
CGG TCC CGG GCT	TCT TCT GAA TGT	GAG GCA ACG TAT	CTT CTC CGG CAA 3810
Arg Ser Arg Ala	Ser Ser Glu Cys	Glu Ala Thr Tyr	Leu Leu Arg Gln
1140	1145	1150	1155
AGC AGC ATC AAT Ser Ser Ile Asn	AGC GCT GAT GGC Ser Ala Asp Gly 1160	TAC AGC TTG TAT Tyr Ser Leu Tyr 1165	CGA TAT CAT TTT 3858 Arg Tyr His Phe 1170
AAC GGA GAA GAG	TTA TTA TTT GAG	GAT ACA TCT CTC	TCC ACG TCA CCA 3906
Asn Gly Glu Glu	Leu Leu Phe Glu	Asp Thr Ser Leu	Ser Thr Ser Pro
117	5	1180	1185
GGG ACA GGA GTC	AGG AAA AAA ACC	Cys Ser Phe Arg	ATA AAG GAA GAG 3954
Gly Thr Gly Val	Arg Lys Lys Thr		Ile Lys Glu Glu
1190	1199		1200
AAG GAC GTG AAA	ACG CAC CTA GTC	CCA GAA TGT CAG	Asn Ser Leu His
Lys Asp Val Lys	Thr His Leu Val	Pro Glu Cys Gln	
1205	1210	121	
CTT TCA CTG GGC	ACA AGC ACA TCA	GCA ACC CCA GAT	GGC AGT CAC CTT 4050
Leu Ser Leu Gly	Thr Ser Thr Ser	Ala Thr Pro Asp	Gly Ser His Leu
1220	1225	1230	1235
GCA GTA GAT GAC Ala Val Asp Asp	TTA AAG AAC GCT Leu Lys Asn Ala 1240	GAA GAG TCA AAA Glu Glu Ser Lys 1245	TTA GGT CCA GAT 4098 Leu Gly Pro Asp 1250
ATT GGG ATT TCA		GAA AGA CAG ACA	GAC TCT AAA AAA 4146
Ile Gly Ile Ser		Glu Arg Gln Thr	Asp Ser Lys Lys
125		1260	1265
GAA GAA ACT ATT	TCC CCA AGT TTA	Asn Lys Thr Asp	GTG ATA CAT GGA 4194
Glu Glu Thr Ile	Ser Pro Ser Leu		Val Ile His Gly
1270	1279		1280
CAG GAC AAA TCA	GAT GTT CAA AAC	ACT CAG CTA ACA	Val Glu Thr Thr
Gln Asp Lys Ser	Asp Val Gln Asn	Thr Gln Leu Thr	
1285	1290	1299	
AAT ATA GAA GGC	ACT ATT TCC TAT	CCC CTG GAA GAA	ACC AAA ATT ACA 4290
Asn Ile Glu Gly	Thr Ile Ser Tyr	Pro Leu Glu Glu	Thr Lys Ile Thr
1300	1305	1310	1315
CGC TAT TTC CCC Arg Tyr Phe Pro	GAT GAA ACG ATC Asp Glu Thr Ile 1320	AAT GCT TGT AAA Asn Ala Cys Lys 1325	ACA ATG AAG TCC 4338 Thr Met Lys Ser 1330
AGA AGC TTC GTC	TAT TCC CGG GGA	AGA AAG CTG GTC	GGT GGG GTT AAC 4386
Arg Ser Phe Val	Tyr Ser Arg Gly	Arg Lys Leu Val	Gly Gly Val Asn
133	5	1340	1345
CAG GAT GTA GAG	TAC AGT TCA ATC	ACG GAC CAG CAA	TTG ACG ACG GAA 4434
Gln Asp Val Glu		Thr Asp Gln Gln	Leu Thr Thr Glu

1350 1355 1360

TGG Trp	CAA Gln 1365	Сув	CAA Gln	GTT Val	CAA Gln	AAG Lys 1370	Ile	ACG Thr	CGC Arg	TCT Ser	CAT His 1375	Ser	ACA Thr	GAT Asp	ATT Ile	4482
CCT Pro 1380	Tyr	ATT Ile	GTG Val	TCG Ser	GAA Glu 1385	GCT Ala	GCA Ala	GTG Val	CAA Gln	GCT Ala 1390	Glu	CAA Gln	AAA Lys	GAG Glu	CAG Gln 1395	4530
TTT Phe	GCA Ala	GAT Asp	ATG Met	CAA Gln 1400	Asp	GAA Glu	CAC His	CAT His	GTC Val 140	Ala	GAA Glu	GCA Ala	ATT Ile	CCT Pro 1410	Arg	4578
ATC Ile	CCT Pro	CGC Arg	TTG Leu 1415	Ser	CTA Leu	ACC Thr	ATT Ile	ACT Thr 1420	Asp	AGA Arg	AAT Asn	GGG Gly	ATG Met 1425	Glu	AAC Asn	4626
TTA Leu	CTG Leu	TCT Ser 1430	Val	AAG Lys	CCA Pro	GAT Asp	CAA Gln 1435	Thr	TTG Leu	GGA Gly	TTC Phe	CCA Pro 1440	Ser	CTC Leu	AGG Arg	4674
TCA Ser	AAA Lys 1445	Ser	TTA Leu	CAT His	GGA Gly	CAT His 1450	Pro	AGG Arg	AAT Asn	GT G Val	AAA Lys 1455	Ser	ATT Ile	CAG Gln	GGA Gly	4722
AAG Lys 1460	Leu	GAC Asp	AG A Arg	TCT Ser	GGA Gly 146	CAT His	GCC Ala	AGT Ser	AGT Ser	GTA Val 1470	Ser	AGC Ser	TTA Leu	GTA Val	ATT Ile 1475	4770
GTG Val	TCT Ser	G GA Gly	ATG Met	ACA Thr 1480	Ala	G AA Glu	G AA Glu	AAA Lys	AAG Lys 1489	Val	AAG Lys	AAA Lys	GAG Glu	AAA Lys 1490	Ala	4818
			ACT Thr 1499	Glu		T AC	GTCT	STTT	r GTT	TCT	AATT	TTT	TTT:	TT		4867
TAAC	CAGTO	CAG A	ACC	ACTAI	AT GO	GTG	CATO	TTC	GCCI	ATCC	TAA	CATO	CA 2	CCA	ATTTCC	4927
TAA	AAACI	ATT :	TCC	CIT												4944

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1497 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro Asp Ser Leu Leu His 1 5 10 15

Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser 20 25 30

Val His Gly Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln

40

Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val Ile Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly Arg Val Cys Ala Ile Gly Ile Ala Pro Trp Gly Ile Val Glu Asn Lys Glu Asp Leu Val Gly 105 Lys Asp Val Thr Arg Val Tyr Gln Thr Met -- Ser Asn Pro Leu Ser Lys 120 Leu Ser Val Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys Leu Arg Arg Leu Leu Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr Arg Leu Gly Gln Gly Val Pro Leu Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser Ile Val Leu Glu Tyr Leu Gln Glu Glu Pro Pro Ile Pro Val Val Ile 200 Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys Tyr Cys Glu Glu Gly Gly Ile Ile Asn Glu Ser Leu Arg Glu Gln Leu Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Asn Lys Ala Gln Ser His Gin Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Glu Leu Val Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Ile Glu Met Ala Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Val Ser Ala Pro Asp Gln 295 Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gin Ile Phe Val Phe Gly Pro His Trp Thr Pro Leu Gly Ser Leu Ala Pro 330 Pro Thr Asp Ser Lys Ala Thr Glu Lys Glu Lys Lys Pro Pro Met Ala

Thr Thr Lys Gly Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Ile Glu Leu 375 Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr 425 Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly 450 Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr 470 Arg Lys Asn Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Pro Lys Ala Leu Lys Leu Leu Gly Met Glu Asp Asp Glu Pro Pro Ala 505 Lys Gly Lys Lys Lys Lys Lys Lys Lys Glu Glu Glu Ile Asp Ile Asp Val Asp Asp Pro Ala Val Ser Arg Phe Gln Tyr Pro Phe His Glu Leu Met Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Val Phe 550 545 Leu Trp Gln Arg Gly Glu Glu Ser Met Ala Lys Ala Leu Val Ala Cys Lys Leu Tyr Lys Ala Met Ala His Glu Ser Ser Glu Ser Asp Leu Val 585 Asp Asp Ile Ser Gln Asp Leu Asp Asn Asn Ser Lys Asp Phe Gly Gln 600 Leu Ala Leu Glu Leu Leu Asp Gln Ser Tyr Lys His Asp Glu Gln Ile Ala Met Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ser Thr 625 Cys Leu Lys Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His 650

Thr Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg Met Arg Lys Asn Pro Gly Leu Lys Val Ile Met Gly Il Leu Leu Pro 680 Pro Thr Ile Leu Phe Leu Glu Phe Arg Thr Tyr Asp Asp Phe Ser Tyr Gin Thr Ser Lys Glu Asn Glu Asp Gly Lys Glu Lys Glu Glu Glu Asn Thr Asp Ala Asn Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn 730 Glu His Lys Lys Gln Arg Ile Ile Pro Ile Gly Thr Lys Ile Cys Lys Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Ile Ser Tyr Leu Gly Tyr Leu Leu Leu Phe Asn Tyr Val Ile Leu Val Arg Met Asp Gly Trp Pro Ser Leu Gln Glu Trp Ile Val Ile Ser Tyr Ile Val Ser Leu Ala Leu Glu Lys Ile Arg Glu Ile Leu Met Ser Glu Pro Gly Lys Leu Ser Gln Lys Ile Lys Val Trp Leu Gln Glu Tyr Trp Asn Ile Thr 820 Asp Leu Val Ala Ile Ser Thr Phe Met Ile Gly Ala Met Ala Thr Arg 840 Ser Val Met Met Ile Gly Lys Met Met Ile Asp Met Leu Tyr Phe Val Val Ile Met Leu Val Val Leu Met Ser Phe Gly Val Ala Arg Gln Ala 870 Ile Leu His Pro Glu Glu Lys Pro Ser Trp Lys Leu Ala Arg Asn Ile 890 Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala Asp Gln 905 Ile Asp Leu Tyr Ala Met Glu Ile Asn Pro Pro Cys Gly Glu Asn Leu 920 Tyr Asp Glu Glu Gly Lys Arg Leu Pro Pro Cys Ile Pro Gly Ala Trp 935 930 Leu Thr Pro Ala Leu Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu 950

- Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val 965 970 975
- Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg Tyr Gln Leu Ile 980 985 985
- Met Thr Phe His Asp Arg Pro Val Leu Pro Pro Pro Met Ile Ile Leu 995 1000 1005
- Ser His Ile Tyr Ile Ile Ile Met Arg Leu Ser Gly Arg Cys Arg Lys 1010 1015 1020
- Lys Arg Glu Gly Asp Gln Glu Glu Arg Asp Arg Gly Leu Lys Leu Phe 1025 1030 1035 1040
- Leu Ser Asp Glu Glu Leu Lys Arg Leu His Glu Phe Glu Glu Gln Cys 1045 1050 1055
- Val Gln Glu His Phe Arg Glu Lys Glu Asp Glu Gln Gln Ser Ser Ser 1060 1065 1070
- Asp Glu Arg Ile Arg Val Thr Ser Glu Arg Val Glu Asn Met Ser Met 1075 1080 1085
- Arg Leu Glu Glu Ile Asn Glu Arg Glu Thr Phe Met Lys Thr Ser Leu 1090 1095 1100
- Gln Thr Val Asp Leu Arg Leu Ala Gln Leu Glu Glu Leu Ser Asn Arg 1105 1110 1115 1120
- Met Val Asn Ala Leu Glu Asn Leu Ala Gly Ile Asp Arg Ser Asp Leu 1125 1130 1135
- Ile Gln Ala Arg Ser Arg Ala Ser Ser Glu Cys Glu Ala Thr Tyr Leu 1140 1145 1150
- Leu Arg Gln Ser Ser Ile Asn Ser Ala Asp Gly Tyr Ser Leu Tyr Arg 1155 1160 1165
- Tyr His Phe Asn Gly Glu Glu Leu Leu Phe Glu Asp Thr Ser Leu Ser 1170 1180
- Thr Ser Pro Gly Thr Gly Val Arg Lys Lys Thr Cys Ser Phe Arg Ile 1185 1190 1195 1200
- Lys Glu Glu Lys Asp Val Lys Thr His Leu Val Pro Glu Cys Gln Asn 1205 1210 1215
- Ser Leu His Leu Ser Leu Gly Thr Ser Thr Ser Ala Thr Pro Asp Gly 1220 1230
- Ser His Leu Ala Val Asp Asp Leu Lys Asn Ala Glu Glu Ser Lys Leu 1235 1240 1245
- Gly Pro Asp Ile Gly Ile Ser Lys Glu Asp Asp Glu Arg Gln Thr Asp 1250 1260

- Ser Lys Lys Glu Glu Thr Ile S r Pro Ser Leu Asn Lys Thr Asp Val
- Ile His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr Gln Leu Thr Val 1290 1285
- Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro Leu Glu Glu Thr 1305
- Lys Ile Thr Arg Tyr Phe Pro Asp Glu Thr Ile Asn Ala Cys Lys Thr 1320
- Met Lys Ser Arg Ser Phe Val Tyr Ser Arg Gly Arg Lys Leu Val Gly 1335
- Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr Asp Gln Gln Leu 1355
- Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr Arg Ser His Ser 1370
- Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val Gln Ala Glu Gln 1385
- Lys Glu Gln Phe Ala Asp Met Gln Asp Glu His His Val Ala Glu Ala 1400 1395
- Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr Asp Arg Asn Gly 1415
- Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr Leu Gly Phe Pro 1430
- Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg Asn Val Lys Ser 1450
- Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser Ser Val Ser Ser 1465 1470
- Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys Lys Val Lys
- Glu Lys Ala Ser Thr Glu Thr Glu Cys 1495 1490
- (2) INFORMATION FOR SEQ ID NO:8:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5055 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA
 - (ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 346..4945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(,				
ACTCATTATA GGG	ntegage ggeeg	CCCGG GCAGGTTTGA	GCTGTGCCCT CTCCATTCCA	60
CTGCTGTGGC AGG	GTCAGAA ATCTT	GGATA GAGAAAACCT	TTTGCAAACG GGAATGTATC	120
TTTGTAATTC CTA	GCACGAA AGACT	CTAAC AGGTGTTGCT	GTGGCCAGTT CACCAACCAG	180
CATATCCCCC CTC	IGCCAAG IGCAA	CACCC AGCAAAAATG	AAGAGGAAAG CAAACAGGTG	240
GAGACTCAGC CTG	AGAAATG GTCTG	TTGCC AAGCACACCC	AGAGCTACCC AACAGATTCC	300
TATGGAGTTC TTG	AATTCCA GGGTGG	GCGGA TATTCCAATA	AAGCC ATG TAT ATC Met Tyr Ile 1	354
CGT GTA TCC TA: Arg Val Ser Ty: 5	r GAC ACC AAG r Asp Thr Lys 10	CCA GAC TCA CTG Pro Asp Ser Leu	CTC CAT CTC ATG GTG Leu His Leu Met Val 15	402
AAA GAT TGG CAG Lys Asp Trp Glo 20	G CTG GAA CTC n Leu Glu Leu 25	CCC AAG CTC TTA Pro Lys Leu Leu 30	ATA TCT GTG CAT GGA Ile Ser Val His Gly 35	450
GGC CTC CAG AAG Gly Leu Gln Ass	C TTT GAG ATG n Phe Glu Met 40	CAG CCC AAG CTG Gln Pro Lys Leu 45	AAA CAA GTC TTT GGG Lys Gln Val Phe Gly 50	498
AAA GGC CTG ATC Lys Gly Leu Ile 59	e Lys Ala Ala	ATG ACC ACC GGG Met Thr Thr Gly 60	GCC TGG ATC TTC ACC Ala Trp Ile Phe Thr 65	546
GGG GGT GTC AGG Gly Gly Val Sec 70	C ACA GGT GTT r Thr Gly Val	ATC AGC CAC GTA Ile Ser His Val 75	GGG GAT GCC TTG AAA Gly Asp Ala Leu Lys 80	594
GAC CAC TCC TCC Asp His Ser Ser 85	C AAG TCC AGA r Lys Ser Arg 90	GGC CGG GTT TGT Gly Arg Val Cys	GCT ATA GGA ATT GCT Ala Ile Gly Ile Ala 95	642
CCA TGG GGC ATC Pro Trp Gly Ilo 100	C GTG GAG AAT B Val Glu Asn 105	AAG GAA GAC CTG Lys Glu Asp Leu 110	GTT GGA AAG GAT GTA Val Gly Lys Asp Val 115	690
ACA AGA GTG TAG Thr Arg Val Tyr	C CAG ACC ATG F Gln Thr Met 120	TCC AAC CCT CTA Ser Asn Pro Leu 125	AGT AAG CTC TCT GTG Ser Lys Leu Ser Val 130	738
CTC AAC AAC TCC Leu Asn Asn Sei 13:	r His Thr His	TTC ATC CTG GCT Phe Ile Leu Ala 140	GAC AAT GGC ACC CTG Asp Asn Gly Thr Leu 145	786
GGC AAG TAT GGG	C GCC GAG GTG	AAG CTG CGA AGG	CTG CTG GAA AAG CAC	834

Gly	Lys	Tyr 150	Gly	Ala	Glu	Val	Lys 155	Lau	Arg	Arg	Leu	Leu 160	Glu	Lys	His	
ATC Ile	TCC Ser 165	CTC Leu	CAG Gln	AAG Lys	ATC Ile	AAC Asn 170	ACA Thr	AGA Arg	CTG Leu	G GG Gly	CAG Gln 175	GGC	GTG Val	CCC Pr	CTC Leu	882
GTG Val 180	GGT Gly	CTC Leu	GTG Val	GTG Val	GAG Glu 185	GGG Gly	GGC Gly	CCT Pro	AAC Asn	GTG Val 190	GTG Val	TCC Ser	ATC Ile	GTC Val	TTG Leu 195	930
G AA Glu	TAC Tyr	CTG Leu	CAA Gln	GAA Glu 200	G AG Glu	CCT Pro	CCC Pro	ATC Ile	CCT Pro 205	GTG Val	GTG Val	ATT Ile	TGT Cys	GAT Asp 210	GGC Gly	978
AGC Ser	GGA Gly	CGT Arg	GCC Ala 215	TCG Ser	GAC Asp	ATC Ile	CTG Leu	TCC Ser 220	TTT Phe	GCG Ala	CAC His	AAG Lys	TAC Tyr 225	TGT Cys	G AA Glu	1026
G AA Glu	GGC Gly	G GA Gly 230	ATA Ile	ATA Ile	AAT Asn	G AG Glu	TCC Ser 235	CTC Leu	AGG Arg	G AG Glu	CAG Gln	CTT Leu 240	CTA Leu	GTT Val	ACC Thr	1074
ATT Ile	CAG Gln 245	AAA Lys	ACA Thr	TTT Phe	AAT Asn	TAT Tyr 250	AAT Asn	AAG Lys	GCA Ala	CAA Gln	TCA Ser 255	CAT His	CAG Gln	CTG Leu	TTT Phe	1122
GCA Ala 260	ATT Ile	ATA Ile	ATG Met	G AG Glu	TGC Cys 265	ATG Met	AAG Lys	AAG Lys	A AA Lys	GAA Glu 270	CTC Leu	GTC Val	ACT Thr	GTG Val	TTC Phe 275	1170
AGA Arg	ATG Met	G GT Gly	TCT Ser	GAG Glu 280	GGC Gly	CAG Gln	CAG Gln	GAC Asp	ATC Ile 285	GAG Glu	ATG Met	GCA Ala	ATT Ile	TTA Leu 290	ACT Thr	1218
GCC Ala	ctg Leu	CTG Leu	AAA Lys 295	GGA Gly	ACA Thr	AAC Asn	GTA Val	TCT Ser 300	GCT Ala	CCA Pro	GAT Asp	CAG Gln	CTG Leu 305	AGC Ser	TTG Leu	1266
GCA Ala	CTG Leu	GCT Ala 310	TGG Trp	AAC Asn	CGC Arg	GTG Val	GAC Asp 315	ATA Ile	GCA Ala	CGA Arg	AGC Ser	CAG Gln 320	ATC Ile	TTT Phe	GTC Val	1314
TTT Phe	GGG Gly 325	CCC Pro	CAC His	TGG Trp	ACG Thr	CCC Pro 330	CTG Leu	GGA Gly	AGC Ser	CTG Leu	GCA Ala 335	CCC Pro	CCG Pro	ACG Thr	GAC Asp	1362
AGC Ser 340	A AA Lys	GCC Ala	ACG Thr	G AG Glu	AAG Lys 345	GAG Glu	AAG Lys	AAG Lys	CCA Pro	CCC Pro 350	ATG Met	GCC Ala	ACC Thr	ACC Thr	AAG Lys 355	1410
GGA Gly	GGA Gly	AG A Arg	G GA Gly	AAA Lys 360	GGG Gly	AAA Lys	GGC Gly	AAG Lys	AAG Lys 365	AAA Lys	GGG Gly	AAA Lys	GTG Val	AAA Lys 370	GAG Glu	1458
GAA Glu	GTG Val	GAG Glu	GAA Glu 375	GAA Glu	ACT Thr	GAC Asp	CCC Pro	CGG Arg 380	AAG. Lys	ATA	GAG Glu	CTG Leu	CTG Leu 385	AAC Asn	TGG Trp	1506

G TG Val	AAT Asn	GCT Ala 390	TTG Leu	G AG Glu	CAA Gln	GCG Ala	ATG Met 395	CTA Leu	GAT Asp	GCT Ala	TTA Leu	GTC Val 400	TTA Leu	GAT Asp	CGT Arg		1554
GTC Val	GAC Asp 405	TTT Phe	GTG V <u>a</u> l	AAG Lys	CTC Leu	CTG Leu 410	ATT Ile	GAA Glu	AAC Asn	GGA Gly	GTG Val 415	AAC Asn	ATG Met	CAA Gln	CAC His	·	1602
TTT Phe 420	CTG Leu	ACC Thr	ATT Ile	CCG Pro	AGG Arg 425	CTG Leu	GA G Glu	GAG Glu	CTT Leu	TAT Tyr 430	AAC Asn	ACA Thr	AGA Arg	ctg Leu	GGT Gly 435		1650
CCA Pro	CCA Pro	AAC Asn	ACA Thr	CTT Leu 440	CAT His	CTG Leu	CTG Leu	GTG Val	AGG Arg 445	Asp	GTG Val	A AA Lys	AAG Lys	AGC Ser 450	AAC Asn		1698
CTT Leu	CCG Pro	CCT Pro	GAT Asp 455	TAC Tyr	CAC His	ATC Ile	AGC Ser	CTC Leu 460	ATA Ile	GAC Asp	ATC Ile	G G Gly	CTC Leu 465	GTG Val	CTG Leu		1746
G AG Glu	TAC Tyr	CTC Leu 470	ATG Met	GGA Gly	G GA Gly	GCC Ala	TAC Tyr 475	CGC Arg	TGC Cys	AAC Asn	TAC Tyr	ACT Thr 480	CGG Arg	AAA Lys	AAC Asn		1794
TTT Phe	CGG Arg 485	ACC Thr	CTT Leu	TAC Tyr	AAC Asn	AAC Asn 490	TTG Leu	TTT Phe	GGA Gly	CCA Pro	AAG Lys 495	AGG Arg	CCT Pro	AAA Lys	GCT Ala		1842
CTT Leu 500	AAA Lys	CTT	CTG Leu	GGA Gly	ATG Met 505	GAA Glu	GAT Asp	GAT Asp	GAG Glu	CCT Pro 510	CCA Pro	GCT Ala	AAA Lys	GGG Gly	AAG Lys 515		1890
A AA Lys	AAA Lys	AAA Lys	AAA Lys	AAG Lys 520	AAA Lys	AAG Lys	GAG Glu	GAA Glu	GAG Glu 525	ATC Ile	GAC Asp	ATT Ile	GAT Asp	GTG Val 530	GAC Asp		1938
G AC Asp	CCT Pro	GCC Ala	GTG Val 535	AGT Ser	CGG Arg	TTC Phe	CAG Gln	TAT Tyr 540	CCC Pro	TTC Phe	CAC His	GAG Glu	CTG Leu 545	ATG Met	GTG Val		1986
TGG Trp	GCA Ala	GTG Val 550	CTG Leu	ATG Met	AAA Lys	CGC Arg	CAG Gln 555	AAA Lys	ATG Met	GCA Ala	GTG Val	TTC Phe 560	CTC	TGG Trp	CAG Gln		2034
CGA Arg	GGG Gly 565	GAA Glu	GAG Glu	AGC Ser	ATG Met	GCC Ala 570	AAG Lys	GCC Ala	CTG Leu	GTG Val	GCC Ala 575	TGC Cys	AAG Lys	CTC Leu	TAC Tyr		2082
AAG Lys 580	GCC Ala	ATG Met	GCC Ala	CAC His	GAG Glu 585	TCC Ser	TCC Ser	GA G Glu	AGT Ser	GAT Asp 590	CTG Leu	GTG Val	GAT Asp	GAC Asp	ATC Ile 595		2130
TCC Ser	CAG Gln	GAC Asp	TTG Leu	GAT Asp 600	AAC Asn	AAT Asn	TCC Ser	AAA Lys	GAC Asp 605	TTC Phe	GGC Gly	CAG Gln	CTT Leu	GCT Ala 610	TTG Leu		2178
G AG Glu	TTA Leu	TTA Leu	GAC Asp	CAG Gln	TCC Ser	TAT Tyr	AAG Lys	CAT His	GAC Asp	G AG Glu	CAG Gln	ATC Ile	GCT Ala	ATG Met	AAA Lys		2226

			615					620					625				
CTC Leu															AAA Lys		2274
CTG Leu																	2322
CAG Gln 660																	2370
AAC Asn																	2418
TTG Leu																	2466
AAG Lys	GAA Glu	AAC Asn 710	GAG Glu	GAT Asp	GGC	AAA Lys	GAA Glu 715	AAA Lys	GAA Glu	GAG Glu	GAA Glu	AAT Asn 720	ACG Thr	GAT Asp	GCA Ala		2514
AAT Asn																	2562
AAA Lys 740																	2610
GCG Ala																	2658
CTG Leu																	2706
TCC (CTC Leu	Gln	G AG Glu	Trp	Ile	Val	Ile	Ser	Tyr	Ile	Val	Ser	Leu	GCG Ala	TTA Leu		2754
GAG																	2802
AAA Lys 820	ATC Ile	A AA Ly s	GTT Val	TGG Trp	CTT Leu 825	CAG Gln	GAG Glu	TAC Tyr	TGG Trp	AAC Asn 830	ATC Ile	ACA Thr	GAT Asp	CTC Lau	GTG Val 835	:	2850
GCC Ala																:	2898

CCC TAC ATG Pro Tyr Met	GGC TAT GGG Gly Tyr Gly 855	CGG GTG	ATC TAC Ile Tyr 860	TGT GTG Cys Val	GAT ATC Asp Ile 865	ATC TTC Ile Phe	2946
TGG TAC ATC Trp Tyr Ile 870	Arg Val Let	GAC ATC Asp Ile 875	TTT GGT Phe Gly	GTC AAC Val Asn	AAG TAT Lys Tyr 880	CTG GGG Leu Gly	2994
CCA TAC GTG Pro Tyr Val 885	ATG ATG ATT Met Met Ile	GGA AAG Gly Lys 890	ATG ATG Met Met	ATC GAC Ile Asp 895	ATG CTG Met Leu	TAC TTT Tyr Phe	3042
GTG GTC ATC Val Val Ile 900	ATG CTG GTG Met Leu Val 909	. Val Leu	Met Ser	TTC GGA Phe Gly -910	GTA GCC Val Ala	CGT CAA Arg Gln 915	3090
GCC ATT CTG Ala Ile Leu	CAT CCA GAG His Pro Glu 920	GAG AAG Glu Lys	CCC TCT Pro Ser 925	TGG AAA Trp Lys	CTG GCC Leu Ala	CGA AAC Arg Asn 930	3138
ATC TTC TAC	ATG CCC TAG Met Pro Tyr 935	TGG ATG	ATC TAT Ile Tyr 940	GGA GAG Gly Glu	GTG TTT Val Phe 945	GCA GAC Ala Asp	3186
CAG ATA GAC Gln Ile Asp 950	Leu Tyr Ala	ATG GAA Met Glu 955	ATT AAT Ile Asn	CCT CCT Pro Pro	TGT GGT Cys Gly 960	GAG AAC Glu Asn	3234
CTA TAT GAT Leu Tyr Asp 965	GAG GAG GGG Glu Glu Gly	AAG CGG Lys Arg 970	CTT CCT Leu Pro	CCC TGT Pro Cys 975	ATC CCC Ile Pro	GGC GCC Gly Ala	3282
TGG CTC ACT Trp Leu Thr 980	CCA GCA CTO Pro Ala Leo 989	Met Ala	TGC TAT Cys Tyr	CTA CTG Leu Leu 990	GTC GCC Val Ala	AAC ATC Asn Ile 995	3330
CTG CTG GTG Leu Leu Val	AAC CTG CTC Asn Leu Leu 1000	ATT GCT	GTG TTC Val Phe 1009	Asn Asn	ACT TTC Thr Phe	TTT GAA Phe Glu 1010	3378
GTA AAA TCA Val Lys Ser	ATA TCC AAG Ile Ser Ass 1015	CAG GTG	TGG AAG Trp Lys 1020	TTC CAG Phe Gln	CGA TAT Arg Tyr 1025	Gln Leu	3426
ATT ATG ACA Ile Met Thr 103	TTT CAT GAO Phe His Asp O	AGG CCA Arg Pro 103	_Val Leu	CCC CCA Pro Pro	CCG ATG Pro Met 1040	ATC ATT	3474
TTA AGC CAC Leu Ser His 1045	ATC TAC ATC	ATC ATT Ile Ile 1050	ATG CGT Met Arg	CTC AGC Leu Ser 1055	Gly Arg	TGC AGG Cys Arg	3522
AAA AAG AGA Lys Lys Arg 1060	GAA GGG GAG Glu Gly Asp 100	Gln Glu	GAA CGG Glu Arg	GAT CGT Asp Arg 1070	GGA TTG Gly Leu	AAG CTC Lys Leu 1075	3570
TTC CTT AGC Phe Leu Ser	GAC GAG GAG Asp Glu Glu	CTA AAG	AGG CTG Arg Leu	CAT GAG His Glu	TTC GAG Phe Glu	GAG CAG Glu Gln	3618

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1080 1085 1090

TGC GTG CAG GAG Cys Val Gln Glu 1099	His Phe Arg Glu	AAG GAG GAT Lys Glu Asp 1100	GAG CAG CAG TCG Glu Gln Gln Ser 11C5	TCC 3666 Ser
AGC GAC GAG CGC Ser Asp Glu Arg 1110	ATC CGG GTC ACT	: Ser Glu Arg	GTT GAA AAT ATG Val Glu Asn Met 1120	TCA 3714 Ser
ATG AGG TTG GAA Met Arg Leu Glu 1125	GAA ATC AAT GAA Glu Ile Asn Glu 1130	A AGA GAA ACT Arg Glu Thr	TTT ATG AAA ACT Phe Met Lys Thr 1135	TCC 3762 Ser
CTG CAG ACT GTT Leu Gln Thr Val 1140	GAC CTT CGA CTT Asp Leu Arg Leu 1145	GCT CAG-CTA Ala Gln Leu 1150	Glu Glu Leu Ser	AAC 3810 Asn 1155
AGA ATG GTG AAT Arg Met Val Asn	GCT CTT GAA AAT Ala Leu Glu Ass 1160	CTT GCG GGA Leu Ala Gly 1165	ATC GAC AGG TCT Ile Asp Arg Ser 1170	Asp
CTG ATC CAG GCA Leu Ile Gln Ala 117	Arg Ser Arg Ala	TCT TCT GAA Ser Ser Glu 1180	TGT GAG GCA ACG Cys Glu Ala Thr 1185	TAT 3906 Tyr
CTT CTC CGG CAA Leu Leu Arg Gln 1190	AGC AGC ATC AAT Ser Ser Ile Ass 115	Ser Ala Asp	GGC TAC AGC TTG Gly Tyr Ser Leu 1200	TAT 3954 Tyr
CGA TAT CAT TTT Arg Tyr His Phe 1205	AAC GGA GAA GAG Asn Gly Glu Glu 1210	ı Leu Leu Phe	GAG GAT ACA TCT Glu Asp Thr Ser 1215	CTC 4002 Leu
TCC ACG TCA CCA Ser Thr Ser Pro 1220	GGG ACA GGA GTO Gly Thr Gly Val 1225	AGG AAA AAA Arg Lys Lys 1230	Thr Cys Ser Phe	CGT 4050 Arg 1235
ATA AAG GAA GAG Ile Lys Glu Glu	AAG GAC GTG AAA Lys Asp Val Lys 1240	A ACG CAC CTA Thr His Leu 1245	GTC CCA GAA TGT Val Pro Glu Cys 1250	Gln
AAC AGT CTT CAC Asn Ser Leu His 125	Leu Ser Leu Gly	ACA AGC ACA Thr Ser Thr 1260	TCA GCA ACC CCA Ser Ala Thr Pro 1265	GAT 4146 Asp
GGC AGT CAC CTT Gly Ser His Leu 1270	GCA GTA GAT GAG Ala Val Asp Asp 127	Leu Lys Asn	GCT GAA GAG TCA Ala Glu Glu Ser 1280	AAA 4194 Lys
TTA GGT CCA GAT Leu Gly Pro Asp 1285	ATT GGG ATT TCI Ile Gly Ile Sei 1290	A AAG GAA GAT Lys Glu Asp	GAT GAA AGA CAG Asp Glu Arg Gln 1295	ACA 4242 Thr
GAC TCT AAA AAA Asp Ser Lys Lys 1300	GAA GAA ACT ATT Glu Glu Thr Ile 1305	TCC CCA AGT Ser Pro Ser 1310	Leu Asn Lys Thr	GAT 4290 Asp 1315

GTG ATA CAT GGA CAG GAC AAA TCA GAT GTT CAA AAC ACT CAG CTA ACA Val lie His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr Gln Leu Thr 1320 1325 1330	4338
GTG GAA ACG ACA AAT ATA GAA GGC ACT ATT TCC TAT CCC CTG GAA GAA Val Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro Leu Glu Glu 1335 1340 1345	4386
ACC AAA ATT ACA CGC TAT TTC CCC GAT GAA ACG ATC AAT GCT TGT AAA Thr Lys Ile Thr Arg Tyr Phe Pro Asp Glu Thr Ile Asn Ala Cys Lys 1350 1355 1360	4434
ACA ATG AAG TCC AGA AGC TTC GTC TAT TCC CGG GGA AGA AAG CTG GTC Thr Met Lys Ser Arg Ser Phe Val Tyr Ser Arg Gly Arg Lys Leu Val 1365	4482
GGT GGG GTT AAC CAG GAT GTA GAG TAC AGT TCA ATC ACG GAC CAA Gly Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr Asp Gln Gln 1380 1385 1390 1395	4530
TTG ACG ACG GAA TGG CAA TGC CAA GTT CAA AAG ATC ACG CGC TCT CAT Leu Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr Arg Ser His 1400 1405 1410	4578
AGC ACA GAT ATT CCT TAC ATT GTG TCG GAA GCT GCA GTG CAA GCT GAG Ser Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val Gln Ala Glu 1415 1420 1425	4626
CAA AAA GAG CAG TTT GCA GAT ATG CAA GAT GAA CAC CAT GTC GCT GAA Gln Lys Glu Gln Phe Ala Asp Met Gln Asp Glu His His Val Ala Glu 1430 1435 1440	4674
GCA ATT CCT CGA ATC CCT CGC TTG TCC CTA ACC ATT ACT GAC AGA AAT Ala Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr Asp Arg Asn 1445 1450 1455	4722
GGG ATG GAA AAC TTA CTG TCT GTG AAG CCA GAT CAA ACT TTG GGA TTC Gly Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr Leu Gly Phe 1460 1465 1470 1475	4770
CCA TCT CTC AGG TCA AAA AGT TTA CAT GGA CAT CCT AGG AAT GTG AAA Pro Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg Asn Val Lys 1480 1485 1490	4818
TCC ATT CAG GGA AAG TTA GAC AGA TCT GGA CAT GCC AGT AGT GTA AGC Ser Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser Ser Val Ser 1495 1500 1505	4866
AGC TTA GTA ATT GTG TCT GGA ATG ACA GCA GAA GAA AAA AAG GTT AAG Ser Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys Lys Val Lys 1510 1515 1520	4914
AAA GAG AAA GCT TCC ACA GAA ACT GAA TGC T AGTCTGTTTT GTTTCTTTAA Lys Glu Lys Ala Ser Thr Glu Thr Glu Cys 1525	4965
TTTTTTTTT TAACAGTCAG AAACCCACTA ATGGGTGTCA TCTTGGCCCA TCCTAAACAC	5 025

(2) INFORMATION FOR SEQ ID NO:9:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1533 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys-Pro Asp Ser Leu Leu His

Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro Lys Leu Leu Ile Ser 20 25 30

Val His Gly Gly Leu Gln Asn Phe Glu Met Gln Pro Lys Leu Lys Gln 35 40 45

Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp 50 55 60

Ile Phe Thr Gly Gly Val Ser Thr Gly Val Ile Ser His Val Gly Asp 65 70 75 80

Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly Arg Val Cys Ala Ile 85 90 95

Gly Ile Ala Pro Trp Gly Ile Val Glu Asn Lys Glu Asp Leu Val Gly 100 105 110

Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser Asn Pro Leu Ser Lys 115 120 125

Leu Ser Val Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn 130 135 140

Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys Leu Arg Arg Leu Leu 145 150 155 160

Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr Arg Leu Gly Gln Gly 165 170 175

Val Pro Leu Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser 180 185 190

Ile Val Leu Glu Tyr Leu Gln Glu Glu Pro Pro Ile Pro Val Val Ile 195 200 205

Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys 210 215 220

Tyr Cys Glu Glu Gly Gly Ile Ile Asn Glu Ser Leu Arg Glu Gln Leu 225 230 235 240 Leu Val Thr Il Gln Lys Thr Phe Asn Tyr Asn Lys Ala Gln Ser His Gln Lau Phe Ala Ile Ile Met Glu Cys Met Lys Lys Glu Lau Val Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Ile Glu Met Ala Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Val Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln Ile Phe Val Phe Gly Pro His Trp Thr Pro Leu Gly Ser Leu Ala Pro Pro Thr Asp Ser Lys Ala Thr Glu Lys Glu Lys Lys Pro Pro Met Ala Thr Thr Lys Gly Gly Arg Gly Lys Gly Lys Lys Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Ile Glu Leu Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val 385 Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly 455 Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg Lys Asn Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg 490 Pro Lys Ala Leu Lys Leu Leu Gly Met Glu Asp Asp Glu Pro Pro Ala Lys Gly Lys Lys Lys Lys Lys Lys Lys Glu Glu Glu Ile Asp Ile Asp Val Asp Asp Pro Ala Val Ser Arg Phe Gln Tyr Pro Phe His Glu 540 535

Leu Met Val Trp Ala Val Leu Met Lys Arg Gln Lys Met Ala Val Phe Leu Trp Gln Arg Gly Glu Glu Ser Met Ala Lys Ala Leu Val Ala Cys Lys Leu Tyr Lys Ala Met Ala His Glu Ser Ser Glu Ser Asp Leu Val Asp Asp Ile Ser Gln Asp Leu Asp Asn Asn Ser Lys Asp Phe Gly Gln Leu Ala Leu Glu Leu Leu Asp Gln Ser Tyr Lys His Asp Glu Gln Ile Ala Met Lys Leu Leu Thr Tyr Glu Leu Lys Asn Trp Ser Asn Ser Thr Cys Leu Lys Leu Ala Val Ala Ala Lys His Arg Asp Phe Ile Ala His 650 Thr Cys Ser Gln Met Leu Leu Thr Asp Met Trp Met Gly Arg Leu Arg Met Arg Lys Asn Pro Gly Leu Lys Val Ile Met Gly Ile Leu Leu Pro Pro Thr Ile Leu Phe Leu Glu Phe Arg Thr Tyr Asp Asp Phe Ser Tyr Gln Thr Ser Lys Glu Asn Glu Asp Gly Lys Glu Lys Glu Glu Glu Asn 710 Thr Asp Ala Asn Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn Glu His Lys Lys Gln Arg Ser Ile Pro Ile Gly Thr Lys Ile Cys Glu Phe Tyr Asn Ala Pro Ile Val Lys Phe Trp Phe Tyr Thr Ile Ser Tyr Leu Gly Tyr Leu Leu Leu Phe Asn Tyr Val Ile Leu Val Arg Met Asp Gly Trp Pro Ser Leu Gln Glu Trp Ile Val Ile Ser Tyr Ile Val Ser 795 790 Leu Ala Leu Glu Lys Ile Arg Glu Ile Leu Met Ser Glu Pro Gly Lys Leu Ser Gln Lys Ile Lys Val Trp Leu Gln Glu Tyr Trp Asn Ile Thr Asp Leu Val Ala Ile Ser Thr Phe Met Ile Gly Ala Ile Leu Arg Leu 840 845 835

Gln Asn Gln Pro Tyr M t Gly Tyr Gly Arg Val Ile Tyr Cys Val Asp Ile Ile Phe Trp Tyr Ile Arg Val Leu Asp Ile Phe Gly Val Asn Lys 870 Tyr Leu Gly Pro Tyr Val Met Met Ile Gly Lys Met Met Ile Asp Met 890 Leu Tyr Phe Val Val Ile Met Leu Val Val Leu Met Ser Phe Gly Val Ala Arg Gln Ala Ile Leu His Pro Glu Glu Lys Pro Ser Trp Lys Leu 920 Ala Arg Asn Ile Phe Tyr Met Pro Tyr Trp Met Ile Tyr Gly Glu Val Phe Ala Asp Gln Ile Asp Leu Tyr Ala Met Glu Ile Asn Pro Pro Cys Gly Glu Asn Leu Tyr Asp Glu Glu Gly Lys Arg Leu Pro Pro Cys Ile Pro Gly Ala Trp Leu Thr Pro Ala Leu Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Val Phe Asn Asn Thr 1000 Phe Phe Glu Val Lys Ser Ile Ser Asn Gln Val Trp Lys Phe Gln Arg 1015 1010 Tyr Gln Leu Ile Met Thr Phe His Asp Arg Pro Val Leu Pro Pro Pro 1035 Met Ile Ile Leu Ser His Ile Tyr Ile Ile Ile Met Arg Leu Ser Gly 1050 1045 Arg Cys Arg Lys Lys Arg Glu Gly Asp Gln Glu Glu Arg Asp Arg Gly 1065 1060 Leu Lys Leu Phe Leu Ser Asp Glu Glu Leu Lys Arg Leu His Glu Phe 1075 Glu Glu Gln Cys Val Gln Glu His Phe Arg Glu Lys Glu Asp Glu Gln 1095 Gln Ser Ser Ser Asp Glu Arg Ile Arg Val Thr Ser Glu Arg Val Glu 1110 1105 Asn Met Ser Met Arg Leu Glu Glu Ile Asn Glu Arg Glu Thr Phe Met

1130

Lys Thr Ser Leu Gln Thr Val Asp Leu Arg Leu Ala Gln Leu Glu Glu 1145

1140

Leu Ser Asn Arg Met Val Asn Ala Leu Glu Asn Leu Ala Gly Ile Asp 1155 1160 1165

Arg Ser Asp Leu Ile Gln Ala Arg Ser Arg Ala Ser Ser Glu Cys Glu 1170 1175 1180

Ala Thr Tyr Leu Leu Arg Gln Ser Ser Ile Asn Ser Ala Asp Gly Tyr 1185 1190 1195 1200

Ser Leu Tyr Arg Tyr His Phe Asn Gly Glu Glu Leu Leu Phe Glu Asp 1205 1210 1215

Thr Ser Leu Ser Thr Ser Pro Gly Thr Gly Val Arg Lys Lys Thr Cys 1220 1225 1230

Ser Phe Arg Ile Lys Glu Glu Lys Asp Val Lys Thr His Leu Val Pro 1235 1240 1245

Glu Cys Gln Asn Ser Leu His Leu Ser Leu Gly Thr Ser Thr Ser Ala 1250 1255 1260

Thr Pro Asp Gly Ser His Leu Ala Val Asp Asp Leu Lys Asn Ala Glu 1265 1270 1275 1280

Glu Ser Lys Leu Gly Pro Asp Ile Gly Ile Ser Lys Glu Asp Asp Glu 1285 1290 1295

Arg Gln Thr Asp Ser Lys Lys Glu Glu Thr Ile Ser Pro Ser Leu Asn 1300 1305 1310

Lys Thr Asp Val Ile His Gly Gln Asp Lys Ser Asp Val Gln Asn Thr 1315 1320 1325

Gin Leu Thr Val Glu Thr Thr Asn Ile Glu Gly Thr Ile Ser Tyr Pro 1330 1340

Leu Glu Glu Thr Lys Ile Thr Arg Tyr Phe Pro Asp Glu Thr Ile Asn 1345 1350 1355 1360

Ala Cys Lys Thr Met Lys Ser Arg Ser Phe Val Tyr Ser Arg Gly Arg 1365 1370 1375

Lys Leu Val Gly Gly Val Asn Gln Asp Val Glu Tyr Ser Ser Ile Thr 1380 1385 1390

Asp Gln Gln Leu Thr Thr Glu Trp Gln Cys Gln Val Gln Lys Ile Thr 1395 1400 1405

Arg Ser His Ser Thr Asp Ile Pro Tyr Ile Val Ser Glu Ala Ala Val 1410 1415 1420

Gin Ala Glu Gin Lys Glu Gin Phe Ala Asp Met Gin Asp Glu His His 1425 1430 1435 1440

Val Ala Glu Ala Ile Pro Arg Ile Pro Arg Leu Ser Leu Thr Ile Thr 1445 1450 1455

Asp Arg Asn Gly Met Glu Asn Leu Leu Ser Val Lys Pro Asp Gln Thr 1460

Leu Gly Phe Pro Ser Leu Arg Ser Lys Ser Leu His Gly His Pro Arg 1475

Asn Val Lys Ser Ile Gln Gly Lys Leu Asp Arg Ser Gly His Ala Ser 1490

Ser Val Ser Ser Leu Val Ile Val Ser Gly Met Thr Ala Glu Glu Lys 1505

Lys Val Lys Lys Glu Lys Ala Ser Thr Glu Thr Glu Cys 1530

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